

SEQUENCE LISTING

<110> Fletcher, Jonathan A.  
Kroll, Todd G.

<120> PAX8-PPARGgamma NUCLEIC ACID MOLECULES  
AND POLYPEPTIDES AND USES THEREOF

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<150> US 60/177,109

<151> 2000-01-20

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<151> 2000-08-14

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Leu Ser Thr His Gln Thr Tyr Pro Val Val Ala Asp Pro His Ser Pro	
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 Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser  
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 Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys  
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 Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys  
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[illegible]

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Glu	Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	Val	Cys	Gly	
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Cys	Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys	Gln	
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Tyr	Cys	Arg	Phe	Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn	Ala	
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Ile	Arg	Phe	Gly	Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu	Ala	
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Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly Glu	
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Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val Glu	
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Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Ser Ile Pro Gly Phe Val	
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Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His	
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Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly Val	
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Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys Ser	
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Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe Ala	
755 760 765	
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Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile Phe	
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Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu Leu	
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Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys Leu	
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Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val Gln	
835 840 845	
cta ctg cag gtg atc aag aag acg gag aca gac atg agt ctt cac ccg	2592
Leu Leu Gln Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His Pro	
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Pro	Lys	Val	Ala	Thr	Pro	Lys	Val	Val	Glu	Lys	Ile	Gly	Asp	Tyr	Lys
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Pro	Cys	Ser	Leu	Ser	Ser	Ser	Ala	Leu	Leu	Asp	Leu	Gln	Gln	Val	Gly
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Ser	Gly	Val	Pro	Phe	Asn	Ala	Phe	Pro	His	Ala	Ala	Ser	Val	Tyr	
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Gly	Gln	Phe	Thr	Gly	Gln	Ala	Leu	Leu	Ser	Gly	Arg	Glu	Met	Val	Gly

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465					470					475					
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Glu	Val	Ala	Ile	Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val	Glu
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Ala	Val	Gln	Glu	Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	Phe	Val
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705					710					715					
Glu	Ile	Ile	Tyr	Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	Gly	Val
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770					775					780					
Ile	Ala	Val	Ile	Ile	Leu	Ser	Gly	Asp	Arg	Pro	Gly	Leu	Leu	Asn	Val
785					790					795					
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Leu	Gln	Lys	Met	Thr	Asp	Leu	Arg	Gln	Ile	Val	Thr	Glu	His	Val	Gln				
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Asn Gln Leu Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val
15              20              25

gtc cgc cag cgc atc gta gac ctg gcc cac cag ggt gta agg ccc tgc
Val Arg Gln Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys
30              35              40              45

gac atc tct cgc cag ctc cgc gtc agc cat ggt tgc gtc agc aag atc
Asp Ile Ser Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile
50              55              60

ctt ggc agg tac tac gag act ggc agc atc cgg cct gga gtg ata ggg
Leu Gly Arg Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly
65              70              75

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Asp	Tyr	Lys	Arg	Gln	Asn	Pro	Thr	Met	Phe	Ala	Trp	Glu	Ile	Arg	Asp	
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cgg	ctc	ctg	gct	gag	ggc	gtc	tgt	gac	aat	gac	act	gtg	ccc	agt	gtc	385
Arg	Leu	Leu	Ala	Glu	Gly	Val	Cys	Asp	Asn	Asp	Thr	Val	Pro	Ser	Val	
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Ser	Ser	Ile	Asn	Arg	Ile	Ile	Arg	Thr	Lys	Val	Gln	Gln	Pro	Phe	Asn	
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Leu	Pro	Met	Asp	Ser	Cys	Val	Ala	Thr	Lys	Ser	Leu	Ser	Pro	Gly	His	
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Thr	Leu	Ile	Pro	Ser	Ser	Ala	Val	Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	
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cag	cct	ggc	agc	gac	aag	agg	aaa	atg	gat	gac	agt	gat	cag	gat	agc	625
Gln	Pro	Gly	Ser	Asp	Lys	Arg	Lys	Met	Asp	Asp	Ser	Asp	Gln	Asp	Ser	
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Cys	Arg	Leu	Ser	Ile	Asp	Ser	Gln	Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	
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tgc	cca	ttt	gag	cgg	cag	cac	tac	cca	gag	gcc	tat	gcc	tcc	ccc	agc	769
Cys	Pro	Phe	Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	
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His	Thr	Lys	Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	
		255				260						265				
acc	ctg	gac	gac	ggg	aag	gcc	acc	ctg	acc	cct	tcc	aac	acg	cca	ctg	865
Thr	Leu	Asp	Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	
270				275						280				285		
ggg	cgc	aac	ctc	tcg	act	cac	cag	acc	tac	ccc	gtg	gtg	gca	gat	cct	913
Gly	Arg	Asn	Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Asp	Pro	
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<210> 14
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<212> PRT
<213> Homo Sapiens
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Gly	Gly	Ala	Phe	Val	Asn	Gly	Arg	Pro	Leu	Pro	Glu	Val	Val	Arg	Gln
			20					25					30		
Arg	Ile	Val	Asp	Leu	Ala	His	Gln	Gly	Val	Arg	Pro	Cys	Asp	Ile	Ser
		35					40					45			
Arg	Gln	Leu	Arg	Val	Ser	His	Gly	Cys	Val	Ser	Lys	Ile	Leu	Gly	Arg
	50					55				60					
Tyr	Tyr	Glu	Thr	Gly	Ser	Ile	Arg	Pro	Gly	Val	Ile	Gly	Gly	Ser	Lys

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<210> 15
<211> 1608
<212> DNA
<213> Homo Sapiens
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aattacagca	aaccctatt	ccatgctggt	atg ggt gaa	act ctg gga	gat tct	114
			Met Gly	Glu Thr	Leu Gly Asp	
			1		5	
cct att gac	cca gaa agc	gat tcc ttc	act gat aca	ctg tct gca	aac	162
Ser						
ata tca caa	gaa atg acc	atg gtt gac	aca gag atg	cca ttc tgg	ccc	210
Pro Ile Asp	Pro Glu Ser	Asp Ser Phe	Thr Asp Thr	Leu Ser Ala	Asn	
10		15		20		
acc aac ttt	ggg atc agc	tcc gtg gat	ctc tcc gta	atg gaa gac	cac	258
Ile Ser Gln	Glu Met Thr	Met Val Asp	Thr Glu Met	Pro Phe Trp	Pro	
25		30		35	40	
tcc cac tcc	ttt gat atc	aag ccc ttc	act act gtt	gac ttc tcc	agc	306
Thr Asn Phe	Gly Ile Ser	Ser Val Asp	Leu Ser Val	Met Glu Asp	His	
	45		50		55	
att tct act	cca cat tac	gaa gac att	cca ttc aca	aga aca gat	cca	354
Ser His Ser	Phe Asp Ile	Lys Pro Phe	Thr Thr Val	Asp Phe Ser	Ser	
	60		65		70	
gtg gtt gca	gat tac aag	tat gac ctg	aaa ctt caa	gag tac caa	agt	402
Ile Ser Thr	Pro His Tyr	Glu Asp Ile	Pro Phe Thr	Arg Thr Asp	Pro	
75		80		85		
gca atc aaa	gtg gag cct	gca tct cca	cct tat tat	tct gag aag	act	450
Val Val Ala	Asp Tyr Lys	Tyr Asp Leu	Lys Leu Gln	Glu Tyr Gln	Ser	
90		95		100		
cag ctc tac	aat aag cct	cat gaa gag	cct tcc aac	tcc ctc atg	gca	498
Ala Ile Lys	Val Glu Pro	Ala Ser Pro	Pro Tyr Tyr	Ser Glu Lys	Thr	
105		110		115	120	
att gaa tgt	cgt gtc tgt	gga gat aaa	gct tct gga	ttt cac tat	gga	546
Gln Leu Tyr	Asn Lys Pro	His Glu Glu	Pro Ser Asn	Ser Leu Met	Ala	
	125		130		135	
gtt cat gct	tgt gaa gga	tgc aag ggt	ttc ttc cgg	aga aca atc	aga	594
Ile Glu Cys	Arg Val Cys	Gly Asp Lys	Ala Ser Gly	Phe His Tyr	Gly	
	140		145		150	
ttg aag ctt	atc tat gac	aga tgt gat	ctt aac tgt	cgg atc cac	aaa	642
Val His Ala	Cys Glu Gly	Cys Lys Gly	Phe Phe Arg	Arg Thr Ile	Arg	
155		160		165		
aaa agt aga	aat aaa tgt	cag tac tgt	cgg ttt cag	aaa tgc ctt	gca	690
Leu Lys Leu	Ile Tyr Asp	Arg Cys Asp	Leu Asn Cys	Arg Ile His	Lys	
170		175		180		

09765111-011304

gtg ggg atg tct cat aat gcc atc agg ttt ggg cgg atg cca cag gcc	738
Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala	
185 190 195 200	
gag aag gag aag ctg ttg gcg gag atc tcc agt gat atc gac cag ctg	786
Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met Pro Gln Ala	
205 210 215	
aat cca gag tcc gct gac ctc cgg gcc ctg gca aaa cat ttg tat gac	834
Glu Lys Glu Lys Leu Leu Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu	
220 225 230	
tca tac ata aag tcc ttc ccg ctg acc aaa gca aag gcg agg gcg atc	882
Asn Pro Glu Ser Ala Asp Leu Arg Ala Leu Ala Lys His Leu Tyr Asp	
235 240 245	
ttg aca gga aag aca aca gac aaa tca cca ttc gtt atc tat gac atg	930
Ser Tyr Ile Lys Ser Phe Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile	
250 255 260	
aat tcc tta atg atg gga gaa gat aaa atc aag ttc aaa cac atc acc	978
Leu Thr Gly Lys Thr Asp Lys Ser Pro Phe Val Ile Tyr Asp Met	
265 270 275 280	
ccc ctg cag gag cag agc aaa gag gtg gcc atc cgc atc ttt cag ggc	1026
Asn Ser Leu Met Met Gly Glu Asp Lys Ile Lys Phe Lys His Ile Thr	
285 290 295	
tgc cag ttt cgc tcc gtg gag gct gtg cag gag atc aca gag tat gcc	1074
Pro Leu Gln Glu Gln Ser Lys Glu Val Ala Ile Arg Ile Phe Gln Gly	
300 305 310	
aaa agc att cct ggt ttt gta aat ctt gac ttg aac gac caa gta act	1122
Cys Gln Phe Arg Ser Val Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala	
315 320 325	
ctc ctc aaa tat gga gtc cac gag atc att tac aca atg ctg gcc tcc	1170
Lys Ser Ile Pro Gly Phe Val Asn Leu Asp Leu Asn Asp Gln Val Thr	
330 335 340	
ttg atg aat aaa gat ggg gtt ctc ata tcc gag ggc caa ggc ttc atg	1218
Leu Leu Lys Tyr Gly Val His Glu Ile Ile Tyr Thr Met Leu Ala Ser	
345 350 355 360	
aca agg gag ttt cta aag agc ctg cga aag cct ttt ggt gac ttt atg	1266
Leu Met Asn Lys Asp Gly Val Leu Ile Ser Glu Gly Gln Gly Phe Met	
365 370 375	
gag ccc aag ttt gag ttt gct gtg aag ttc aat gca ctg gaa tta gat	1314
Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Gly Asp Phe Met	
380 385 390	
gac agc gac ttg gca ata ttt att gct gtc att att ctc agt gga gac	1362
Glu Pro Lys Phe Glu Phe Ala Val Lys Phe Asn Ala Leu Glu Leu Asp	
395 400 405	

09765111 011301

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Phe	Thr	Asp	Thr	Leu	Ser	Ala	Asn	Ile	Ser	Gln	Glu	Met	Thr	Met	Val
			20					25					30		
Asp	Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser	Ser	Val
		35					40					45			
Asp	Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile	Lys	Pro
	50					55					60				
Phe 65	Thr	Thr	Val	Asp	Phe	Ser	Ser	Ile	Ser	Thr	Pro	His	Tyr	Glu	Asp
				70						75				80	
Ile	Pro	Phe	Thr	Arg	Thr	Asp	Pro	Val	Val	Ala	Asp	Tyr	Lys	Tyr	Asp
				85					90					95	
Leu	Lys	Leu	Gln	Glu	Tyr	Gln	Ser	Ala	Ile	Lys	Val	Glu	Pro	Ala	Ser
			100					105					110		
Pro	Pro	Tyr	Tyr	Ser	Glu	Lys	Thr	Gln	Leu	Tyr	Asn	Lys	Pro	His	Glu
		115					120					125			
Glu	Pro	Ser	Asn	Ser	Leu	Met	Ala	Ile	Glu	Cys	Arg	Val	Cys	Gly	Asp
	130					135					140				
Lys 145	Ala	Ser	Gly	Phe	His	Tyr	Gly	Val	His	Ala	Cys	Glu	Gly	Cys	Lys
				150						155				160	
Gly	Phe	Phe	Arg	Arg	Thr	Ile	Arg	Leu	Lys	Leu	Ile	Tyr	Asp	Arg	Cys
			165						170					175	
Asp	Leu	Asn	Cys	Arg	Ile	His	Lys	Lys	Ser	Arg	Asn	Lys	Cys	Gln	Tyr
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<210> 17
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<212> DNA
<213> Homo Sapiens
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21

18

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<210> 19
<211> 20
<212> DNA
<213> Homo Sapiens

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<210> 20
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<210> 22
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tgagggcctg cagccggccg gccagggcag cggcaggcgc ggcccggacc tacggggagga      120
agccccgagc cctcggcggg ctgcgagcga ctccccggcg atg cct cac aac tcc          175
                                         Met Pro His Asn
                                         1

atc aga tct ggc cat gga ggg ctg aac cag ctg gga ggg gcc ttt gtg          223
Ser
5

aat ggc aga cct ctg ccg gaa gtg gtc cgc cag cgc atc gta gac ctg          271
Ile Arg Ser Gly His Gly Gly Leu Asn Gln Leu Gly Gly Ala Phe Val
                        10                        15                        20

gcc cac cag ggt gta agg ccc tgc gac atc tct cgc cag ctc cgc gtc          319
Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln Arg Ile Val Asp Leu
                        25                        30                        35

agc cat ggc tgc gtc agc aag atc ctt ggc agg tac tac gag act ggc          367
Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser Arg Gln Leu Arg Val
                        40                        45                        50

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agc Ser	atc His	cgg Gly	cct Cys	gga Val	gtg Ser	ata Lys	ggg Ile	ggc Leu	tcc Gly	aag Arg	ccc Tyr	aag Tyr	gtg Glu	gcc Thr	acc Gly	415
55						60				65						
ccc Ser	aag Ile	gtg Arg	gtg Pro	gag Gly	aag Val	att Ile	ggg Gly	gac Gly	tac Ser	aaa Lys	cgc Pro	cag Lys	aac Val	cct Ala	acc Thr	463
70				75						80				85		
atg Pro	ttt Lys	gcc Val	tgg Val	gag Glu	atc Lys	cga Ile	gac Gly	cgg Asp	ctc Tyr	ctg Lys	gct Arg	gag Gln	ggc Asn	gtc Pro	tgt Thr	511
				90				95						100		
gac Met	aat Phe	gac Ala	act Trp	gtg Glu	ccc Ile	agt Arg	gtc Asp	agc Arg	tcc Leu	att Leu	aat Ala	aga Glu	atc Gly	atc Val	cgg Cys	559
		105						110				115				
acc Asp	aaa Asn	gtg Asp	cag Thr	caa Val	cca Pro	ttc Ser	aac Val	ctc Ser	cct Ser	atg Ile	gac Asn	agc Arg	tgc Ile	gtg Ile	gcc Arg	607
		120				125						130				
acc Thr	aag Lys	tcc Val	ctg Gln	agt Gln	ccc Pro	gga Phe	cac Asn	acg Leu	ctg Pro	atc Met	ccc Asp	agc Ser	tca Cys	gct Val	gta Ala	655
135						140				145						
act Thr	ccc Lys	ccg Ser	gag Leu	tca Ser	ccc Pro	cag Gly	tcg His	gat Thr	tcc Leu	ctg Ile	ggc Pro	tcc Ser	acc Ser	tac Ala	tcc Val	703
150				155						160				165		
atc Thr	aat Pro	ggg Pro	ctc Glu	ctg Ser	ggc Pro	atc Gln	gct Ser	cag Asp	cct Ser	ggc Leu	agc Gly	gac Ser	aag Thr	agg Tyr	aaa Ser	751
				170				175						180		
atg Ile	gat Asn	gac Gly	agt Leu	gat Leu	cag Gly	gat Ile	agc Ala	tgc Gln	cga Pro	cta Gly	agc Ser	att Asp	gac Lys	tca Arg	cag Lys	799
		185						190				195				
agc Met	agc Asp	agc Asp	agc Ser	gga Asp	ccc Gln	cga Asp	aag Ser	cac Cys	ctt Arg	cgc Leu	acg Ser	gat Ile	gcc Asp	ttc Ser	agc Gln	847
200		205				205						210				
cag Ser	cac Ser	cac Ser	ctc Ser	gag Gly	ccg Pro	ctc Arg	gag Lys	tgc His	cca Leu	ttt Arg	gag Thr	cgg Asp	cag Ala	cac Phe	tac Ser	895
215						220				225						
cca Gln	gag His	gcc His	tat Leu	gcc Glu	tcc Pro	ccc Leu	agc Glu	cac Cys	acc Pro	aaa Phe	ggc Glu	gag Arg	cag Gln	ggc His	ctc Tyr	943
230				235						240				245		
tac Pro	ccg Glu	ctg Ala	ccc Tyr	ttg Ala	ctc Ser	aac Pro	agc Ser	acc His	ctg Thr	gac Lys	gac Gly	ggg Glu	aag Gln	gcc Gly	acc Leu	991
				250				255						260		
ctg Tyr	acc Pro	cct Leu	tcc Pro	aac Leu	acg Leu	cca Asn	ctg Ser	ggg Thr	cgc Leu	aac Asp	ctc Asp	tcg Gly	act Lys	cac Ala	cag Thr	1039
		265						270				275				

acc tac ccc gtg gtg gca ggg cga gag atg gtg ggg ccc acg ctg ccc	1087
Leu Thr Pro Ser Asn Thr Pro Leu Gly Arg Asn Leu Ser Thr His Gln	
280 285 290	
gga tac cca ccc cac atc ccc acc agc gga cag ggc agc tat gcc tcc	1135
Thr Tyr Pro Val Val Ala Gly Arg Glu Met Val Gly Pro Thr Leu Pro	
295 300 305	
tct gcc atc gca ggc atg gtg gca gaa atg acc atg gtt gac aca gag	1183
Gly Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly Ser Tyr Ala Ser	
310 315 320 325	
atg cca ttc tgg ccc acc aac ttt ggg atc agc tcc gtg gat ctc tcc	1231
Ser Ala Ile Ala Gly Met Val Ala Glu Met Thr Met Val Asp Thr Glu	
330 335 340	
gta atg gaa gac cac tcc cac tcc ttt gat atc aag ccc ttc act act	1279
Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser Ser Val Asp Leu Ser	
345 350 355	
gtt gac ttc tcc agc att tct act cca cat tac gaa gac att cca ttc	1327
Val Met Glu Asp His Ser His Ser Phe Asp Ile Lys Pro Phe Thr Thr	
360 365 370	
aca aga aca gat cca gtg gtt gca gat tac aag tat gac ctg aaa ctt	1375
Val Asp Phe Ser Ser Ile Ser Thr Pro His Tyr Glu Asp Ile Pro Phe	
375 380 385	
caa gag tac caa agt gca atc aaa gtg gag cct gca tct cca cct tat	1423
Thr Arg Thr Asp Pro Val Val Ala Asp Tyr Lys Tyr Asp Leu Lys Leu	
390 395 400 405	
tat tct gag aag act cag ctc tac aat aag cct cat gaa gag cct tcc	1471
Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro Ala Ser Pro Pro Tyr	
410 415 420	
aac tcc ctc atg gca att gaa tgt cgt gtc tgt gga gat aaa gct tct	1519
Tyr Ser Glu Lys Thr Gln Leu Tyr Asn Lys Pro His Glu Glu Pro Ser	
425 430 435	
gga ttt cac tat gga gtt cat gct tgt gaa gga tgc aag ggt ttc ttc	1567
Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys Gly Asp Lys Ala Ser	
440 445 450	
cgg aga aca atc aga ttg aag ctt atc tat gac aga tgt gat ctt aac	1615
Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe	
455 460 465	
tgt cgg atc cac aaa aaa agt aga aat aaa tgt cag tac tgt cgg ttt	1663
Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp Arg Cys Asp Leu Asn	
470 475 480 485	
cag aaa tgc ctt gca gtg ggg atg tct cat aat gcc atc agg ttt ggg	1711
Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys Gln Tyr Cys Arg Phe	
490 495 500	

cg	g	at	g	cca	cag	gcc	gag	aag	gag	aag	ctg	ttg	g	g	gag	atc	tcc	agt	1759
Gln	Lys	Cys	Leu	Ala	Val	Gly	Met	Ser	His	Asn	Ala	Ile	Arg	Phe	Gly				
			505					510							515				
gat	atc	gac	cag	ctg	aat	cca	gag	tcc	gct	gac	ctc	cg	g	gcc	ctg	gca			1807
Arg	Met	Pro	Gln	Ala	Glu	Lys	Glu	Lys	Leu	Leu	Ala	Glu	Ile	Ser	Ser				
			520				525					530							
aaa	cat	ttg	tat	gac	tca	tac	ata	aag	tcc	ttc	ccg	ctg	acc	aaa	gca				1855
Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp	Leu	Arg	Ala	Leu	Ala				
			535			540					545								
aag	gc	agg	gc	atc	ttg	aca	gga	aag	aca	aca	gac	aaa	tca	cca	ttc				1903
Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser	Phe	Pro	Leu	Thr	Lys	Ala				
					555					560					565				
gtt	atc	tat	gac	atg	aat	tcc	tta	atg	atg	gga	gaa	gat	aaa	atc	aag				1951
Lys	Ala	Arg	Ala	Ile	Leu	Thr	Gly	Lys	Thr	Thr	Asp	Lys	Ser	Pro	Phe				
					570					575					580				
ttc	aaa	cac	atc	acc	ccc	ctg	cag	gag	cag	agc	aaa	gag	gtg	gcc	atc				1999
Val	Ile	Tyr	Asp	Met	Asn	Ser	Leu	Met	Met	Gly	Glu	Asp	Lys	Ile	Lys				
				585				590						595					
cg	atc	ttt	cag	ggc	tgc	cag	ttt	cg	tcc	gtg	gag	gct	gtg	cag	gag				2047
Phe	Lys	His	Ile	Thr	Pro	Leu	Gln	Glu	Gln	Ser	Lys	Glu	Val	Ala	Ile				
			600				605					610							
atc	aca	gag	tat	gcc	aaa	agc	att	cct	ggt	ttt	gta	aat	ctt	gac	ttg				2095
Arg	Ile	Phe	Gln	Gly	Cys	Gln	Phe	Arg	Ser	Val	Glu	Ala	Val	Gln	Glu				
				615			620							625					
aac	gac	caa	gta	act	ctc	ctc	aaa	tat	gga	gtc	cac	gag	atc	att	tac				2143
Ile	Thr	Glu	Tyr	Ala	Lys	Ser	Ile	Pro	Gly	Phe	Val	Asn	Leu	Asp	Leu				
				630			635				640				645				
aca	atg	ctg	gcc	tcc	ttg	atg	aat	aaa	gat	ggg	gtt	ctc	ata	tcc	gag				2191
Asn	Asp	Gln	Val	Thr	Leu	Leu	Lys	Tyr	Gly	Val	His	Glu	Ile	Ile	Tyr				
				650					655						660				
ggc	caa	ggc	ttc	atg	aca	agg	gag	ttt	cta	aag	agc	ctg	cga	aag	cct				2239
Thr	Met	Leu	Ala	Ser	Leu	Met	Asn	Lys	Asp	Gly	Val	Leu	Ile	Ser	Glu				
				665				670							675				
ttt	ggt	gac	ttt	atg	gag	ccc	aag	ttt	gag	ttt	gct	gtg	aag	ttc	aat				2287
Gly	Gln	Gly	Phe	Met	Thr	Arg	Glu	Phe	Leu	Lys	Ser	Leu	Arg	Lys	Pro				
			680				685								690				
gca	ctg	gaa	tta	gat	gac	agc	gac	ttg	gca	ata	ttt	att	gct	gtc	att				2335
Phe	Gly	Asp	Phe	Met	Glu	Pro	Lys	Phe	Glu	Phe	Ala	Val	Lys	Phe	Asn				
				695			700								705				
att	ctc	agt	gga	gac	cg	cca	ggt	ttg	ctg	aat	gtg	aag	ccc	att	gaa				2383
Ala	Leu	Glu	Leu	Asp	Asp	Ser	Asp	Leu	Ala	Ile	Phe	Ile	Ala	Val	Ile				
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<210> 23
<211> 811
<212> PRT
<213> Homo Sapiens

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Gly Gly Ala Phe Val Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln
20      25      30
Arg Ile Val Asp Leu Ala His Gln Gly Val Arg Pro Cys Asp Ile Ser
35      40      45
Arg Gln Leu Arg Val Ser His Gly Cys Val Ser Lys Ile Leu Gly Arg
50      55      60
Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys
65      70      75      80
Pro Lys Val Ala Thr Pro Lys Val Val Glu Lys Ile Gly Asp Tyr Lys
85      90      95
Arg Gln Asn Pro Thr Met Phe Ala Trp Glu Ile Arg Asp Arg Leu Leu
100     105     110
Ala Glu Gly Val Cys Asp Asn Asp Thr Val Pro Ser Val Ser Ser Ile
115     120     125
Asn Arg Ile Ile Arg Thr Lys Val Gln Gln Pro Phe Asn Leu Pro Met
130     135     140
Asp Ser Cys Val Ala Thr Lys Ser Leu Ser Pro Gly His Thr Leu Ile
145     150     155     160
Pro Ser Ser Ala Val Thr Pro Pro Glu Ser Pro Gln Ser Asp Ser Leu
165     170     175
Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly
180     185     190
Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu
195     200     205
Ser Ile Asp Ser Gln Ser Ser Ser Ser Gly Pro Arg Lys His Leu Arg
210     215     220

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Thr	Asp	Ala	Phe	Ser	Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe
225					230					235					240
Glu	Arg	Gln	His	Tyr	Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys
				245					250						255
Gly	Glu	Gln	Gly	Leu	Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp
			260					265					270		
Asp	Gly	Lys	Ala	Thr	Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn
		275					280					285			
Leu	Ser	Thr	His	Gln	Thr	Tyr	Pro	Val	Val	Ala	Gly	Arg	Glu	Met	Val
	290					295					300				
Gly	Pro	Thr	Leu	Pro	Gly	Tyr	Pro	Pro	His	Ile	Pro	Thr	Ser	Gly	Gln
305					310					315					320
Gly	Ser	Tyr	Ala	Ser	Ser	Ala	Ile	Ala	Gly	Met	Val	Ala	Glu	Met	Thr
				325					330						335
Met	Val	Asp	Thr	Glu	Met	Pro	Phe	Trp	Pro	Thr	Asn	Phe	Gly	Ile	Ser
			340					345					350		
Ser	Val	Asp	Leu	Ser	Val	Met	Glu	Asp	His	Ser	His	Ser	Phe	Asp	Ile
		355					360						365		
Lys	Pro	Phe	Thr	Thr	Val	Asp	Phe	Ser	Ser	Ile	Ser	Thr	Pro	His	Tyr
	370					375						380			
Glu	Asp	Ile	Pro	Phe	Thr	Arg	Thr	Asp	Pro	Val	Val	Ala	Asp	Tyr	Lys
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Ala	Glu	Ile	Ser	Ser	Asp	Ile	Asp	Gln	Leu	Asn	Pro	Glu	Ser	Ala	Asp
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Met Pro His Asn Ser  
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Asn Gly Arg Pro Leu Pro Glu Val Val Arg Gln Arg Ile Val Asp Leu  
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gac	aat	gac	act	gtg	ccc	agt	gtc	agc	tcc	att	aat	aga	atc	atc	cgg	559	
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Thr	Pro	Pro	Glu	Ser	Pro	Gln	Ser	Asp	Ser	Leu	Gly	Ser	Thr	Tyr	Ser		
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Ile	Asn	Gly	Leu	Leu	Gly	Ile	Ala	Gln	Pro	Gly	Ser	Asp	Lys	Arg	Lys		
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Ser	Ser	Ser	Ser	Gly	Pro	Arg	Lys	His	Leu	Arg	Thr	Asp	Ala	Phe	Ser		
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Gln	His	His	Leu	Glu	Pro	Leu	Glu	Cys	Pro	Phe	Glu	Arg	Gln	His	Tyr		
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Pro	Glu	Ala	Tyr	Ala	Ser	Pro	Ser	His	Thr	Lys	Gly	Glu	Gln	Gly	Leu		
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Tyr	Pro	Leu	Pro	Leu	Leu	Asn	Ser	Thr	Leu	Asp	Asp	Gly	Lys	Ala	Thr		
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Leu	Thr	Pro	Ser	Asn	Thr	Pro	Leu	Gly	Arg	Asn	Leu	Ser	Thr	His	Gln		
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Thr	Tyr	Pro	Val	Val	Ala	Asp	Pro	His	Ser	Pro	Leu	Ala	Ile	Lys	Gln		
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Gln Ala Leu Leu Ser Gly Arg Glu Met Val Gly Pro Thr Leu Pro Gly	
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Tyr Pro Pro His Ile Pro Thr Ser Gly Gln Gly Ser Tyr Ala Ser Ser	
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Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala Trp Gly Phe Pro Asn	
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 Tyr Tyr Glu Thr Gly Ser Ile Arg Pro Gly Val Ile Gly Gly Ser Lys  
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 Gly Ser Thr Tyr Ser Ile Asn Gly Leu Leu Gly Ile Ala Gln Pro Gly  
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 Ser Asp Lys Arg Lys Met Asp Asp Ser Asp Gln Asp Ser Cys Arg Leu  
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 Thr Asp Ala Phe Ser Gln His His Leu Glu Pro Leu Glu Cys Pro Phe  
 225 230 235 240  
 Glu Arg Gln His Tyr Pro Glu Ala Tyr Ala Ser Pro Ser His Thr Lys  
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 Gly Glu Gln Gly Leu Tyr Pro Leu Pro Leu Leu Asn Ser Thr Leu Asp  
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Leu	Arg	Gln	Ala	Leu	Ala	Lys	His	Leu	Tyr	Asp	Ser	Tyr	Ile	Lys	Ser		
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Asn Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu	
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Glu Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala	
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<212> DNA
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20

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[illegible]

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[illegible]

115

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 Phe Thr Asp Thr Leu Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr  
           20                  25                  30  
 Ser Gly Asn Ala Tyr Gly His Thr Pro Tyr Ser Ser Tyr Ser Glu Ala  
           35                  40                  45  
 Trp Arg Phe Pro Asn Ser Ser Leu Leu Ser Ser Pro Tyr Tyr Tyr Ser  
       50                  55                  60  
 Ser Thr Ser Arg Pro Ser Ala Pro Pro Thr Thr Ala Thr Ala Phe Asp  
   65                  70                  75                  80  
 His Leu

<210> 42  
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<400> 42  
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 Ser Ala Asn Ile Ser Gln Glu Xaa Pro His Ser Pro Phe Ala  
   1                  5                  10

43

<210> 43  
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   1                  5                  10

<210> 44  
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007541.01201

$\langle 220 \rangle$ 

<221> CDS

<400> 44

43

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<213> Homo Sapiens

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<210> 47

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<400> 47

Ser Ala Asn Ile Ser Gln Glu Xaa Ser Glu Tyr Ser Gly Asn  
1 5 10